

1/9

Input file Fbh2786c.seq; Output File 2786.trans
Sequence length 2459

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|---|-----|-----|-----|-----|----|---|---|---|---|-----------|
| CGCGCCGCGTCGACCTCCCCTCGGGTTCGCGGCCCGCGCGGTGAGCAACGGCTCTGCGGCC | ATG | GCG | AGC | GGC | | | | | | 12 73 |
| E H S P G S G A A R R P L H S A ¹⁶² O A V D | | | | | | | | | | 24 |
| GAG CAT TCC CCC GGC AGC GGC GCG GCC CGG CGG CCG CTG CAC TCC GCG CAG GCT GTG GAC | | | | | | | | | | 72 133 |
| V A S A S N F R A F E L L H L H L D L R | | | | | | | | | | 44 |
| GTG GCC TCG GCC TCC AAC TTC CGG GCC TTT GAG CTG CTG CAC TTG CAC CTG GAC CTG CGG | | | | | | | | | | 132 193 |
| A E F G P P G P G A G S R G L S G T A V | | | | | | | | | | 64 |
| GCT GAG TTC GCG CCT CCA GGG CCC GGC GCA GGG AGC CGG GGG CTG AGC GGC ACC GCG GTC | | | | | | | | | | 192 253 |
| L D L R C L E P E G A A A E L R L D S H P | | | | | | | | | | 84 |
| CTG GAC CTG CGC TGC CTG GAG CCC GAG GGC GCC GCC AGG CTG CGG CTG GAC TCG CAC CCG | | | | | | | | | | 252 313 |
| C L E V T A A A L R R E R P G S E E P P | | | | | | | | | | 104 |
| TGC CTG GAG GTG ACG GCG GCG GCG CTG CGG CGG GAG CGG CCC GGC TCG GAG GAG CCG CCT | | | | | | | | | | 312 373 |
| A E P V S F Y T O P F S H Y G O A L C V | | | | | | | | | | 124 |
| GCG GAG CCC GTG AGC TTC TAC ACG CAG CCC TTC TCG CAC TAT GGC CAG GCC CTG TGC GTG | | | | | | | | | | 372 433 |
| S F P O P C R A A E R L O V L L T Y R V | | | | | | | | | | 144 |
| TCC TTC CCG CAG CCC TGC CGC GCC GCC GAG CGC CTC CAG GTG CTG CTC ACC TAC CGC GTC | | | | | | | | | | 432 493 |
| G E G P G V C W L A P E O T A G K K K P | | | | | | | | | | 164 |
| GGG GAG GGA CCC GGG GTT TGC TGG TTG GCT CCC GAG CAG ACA GCA GGA AAG AAG AAG CCC | | | | | | | | | | 492 553 |
| F V Y T O G O A V L N R A F F P C F D T | | | | | | | | | | 184 |
| TTC GTG TAC ACC CAG GGC CAG GCT GTC CTA AAC CGG GCC TTC TTC CCT TGC TTC GAC ACG | | | | | | | | | | 552 613 |
| P A V K Y K Y S A L I E V P D G F T A V | | | | | | | | | | 204 |
| CCT GCT GTT AAA TAC AAG TAT TCA GCT CTT ATT GAG GTC CCA GAT GGC TTC ACA GCT GTG | | | | | | | | | | 612 673 |
| M S A S T W E K R G P N K F F F O M C O | | | | | | | | | | 224 |
| ATG AGT GCT AGC ACC TGG GAG AAG AGA GGT CCA AAT AAG TTC TTC TTC CAG ATG TGT CAG | | | | | | | | | | 672 733 |
| P I P S Y L I A L A I G D L V S A E V G | | | | | | | | | | 244 |
| CCC ATC CCC TCC TAT CTG ATA GCT TTG GCC ATC GGA GAT CTG GTT TCG GCT GAA GTT GGA | | | | | | | | | | 732 793 |
| P R S R V W A E P C L I D A A N E E Y N | | | | | | | | | | 264 |
| CCC AGG AGC CGG GTG TGG GCT GAG CCC TGC CTG ATT GAT GCT GCC AAT GAG GAG TAC AAC | | | | | | | | | | 792 853 |
| G V I E E F L A T G E K L F G P Y V W G | | | | | | | | | | 284 |
| GGG GTG ATA GAA GAA TTT TTG GCA ACA GGA GAG AAG CTT TTT GGA CCT TAT GTT TGG GGA | | | | | | | | | | 852 913 |
| R Y D L L F M P P S F P F G G M E N P C | | | | | | | | | | 304 |
| AGG TAT GAC TTG CTC TTC ATG CCA CCG TCC TTT CCA TTT GGA GGA ATG GAG AAC CCT TGT | | | | | | | | | | 912 973 |
| L T F V T P C L A G D R S L A D V I I | | | | | | | | | | 324 |
| CTG ACC TTT GTC ACC CCC TGC CTG CTA GCT GGG GAC CGC TCC TTG GCA GAT GTC ATC ATC | | | | | | | | | | 972 1033 |
| H E I S H S W F G N L V T N A N W G E F | | | | | | | | | | 344 |
| CAT GAG ATC TCC CAC AGT TGG TTT GGG AAC CTG GTC ACC AAC GCC AAC TGG GGT GAA TTC | | | | | | | | | | 1032 1093 |
| W L N E G F T M Y A O R R I S T I L F G | | | | | | | | | | 364 |
| TGG CTC AAT GAA GGT TTC ACC ATG TAC GCC CAG AGG AGG ATC TCC ACC ATC CTC TTT GGC | | | | | | | | | | 1092 1153 |
| A A Y T C L E A A T G R A L L R O H M D | | | | | | | | | | 384 |
| GCT GCG TAC ACC TGC TTG GAG GCT GCA ACG GGG CGG GCT CTG CTG CGT CAA CAC ATG GAC | | | | | | | | | | 1152 1213 |
| I T G E E N P L N K L R V K I E P G V D | | | | | | | | | | 404 |
| ATC ACT GGA GAG GAA AAC CCA CTC AAC AAG CTC CGC GTG AAG ATT GAA CCA GGC GTT GAC | | | | | | | | | | 1212 1273 |
| P D D T Y N E T P Y E K G F C F V S Y L | | | | | | | | | | 424 |
| CCG GAC GAC ACC TAT AAT GAG ACC CCC TAC GAG AAA GGT TTC TGC TTT GTC TCA TAC CTG | | | | | | | | | | 1272 1333 |
| A H L V G D O D O F D S F L K A Y V H E | | | | | | | | | | 444 |
| GCC CAC TTG GTG GGT GAT CAG GAT CAG TTT GAC AGT TTT CTC AAG GCC TAT GTG CAT GAA | | | | | | | | | | 1332 1393 |
| F K F R S I L A D D F L D F Y L E Y F P | | | | | | | | | | 464 |
| TTC AAA TTC CGA AGC ATC TTA GCC GAT GAC TTT CTG GAC TTC TAC TTG GAA TAT TTC CCT | | | | | | | | | | 1392 1453 |

FIG. 1A.

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| | | | | | | | | | | | | | | | | | | | | |
|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----------|
| E | L | K | K | K | R | V | D | I | I | P | G | F | E | F | D | R | W | L | N | 484 |
| GAG | CTT | AAG | AAA | AAG | AGA | GTG | GAT | ATC | ATT | CCA | GGT | TTT | GAG | TTT | GAT | CGA | TGG | CTG | AAT | 1452 1513 |
| T | P | G | W | P | P | Y | L | P | D | L | S | P | G | D | S | L | M | K | P | 504 |
| ACC | CCC | GGC | TGG | CCC | CCG | TAC | CTC | CCT | GAT | CTC | TCC | CCT | GGG | GAC | TCA | CTC | ATG | AAG | CCT | 1512 1573 |
| A | E | E | L | A | O | L | W | A | A | E | E | L | D | M | K | A | I | E | A | 524 |
| GCT | GAA | GAG | CTA | GCC | CAA | CTG | TGG | GCA | GCC | GAG | GAG | CTG | GAC | ATG | AAG | GCC | ATT | GAA | GCC | 1572 1633 |
| V | A | I | S | P | W | K | T | Y | O | L | V | Y | F | L | D | K | I | L | O | 544 |
| GTG | GCC | ATC | TCT | CCC | TGG | AAG | ACC | TAC | CAG | CTG | GTC | TAC | TTC | CTG | GAT | AAG | ATC | CTC | CAG | 1632 1693 |
| K | S | P | L | P | P | G | N | V | K | K | L | G | D | T | Y | P | S | I | S | 564 |
| AAA | TCC | CCT | CTC | CCT | CCT | GGG | AAT | GTG | AAA | AAA | CTT | GGA | GAC | ACA | TAC | CCA | AGT | ATC | TCA | 1692 1753 |
| N | A | R | N | A | E | L | R | L | R | W | G | O | I | V | L | K | N | D | H | 584 |
| AAT | GCC | CGG | AAT | GCA | GAG | CTC | CGG | CTG | CGA | TGG | GGC | CAA | ATC | GTC | CTT | AAG | AAC | GAC | CAC | 1752 1813 |
| O | E | D | F | W | K | V | K | E | F | L | H | N | O | G | K | O | R | Y | T | 604 |
| CAG | GAA | GAT | TTC | TGG | AAA | GTG | AAG | GAG | TTC | CTG | CAT | AAC | CAG | GGG | AAG | CAG | AAG | TAT | ACA | 1812 1873 |
| L | P | L | Y | H | A | M | M | G | G | S | E | V | A | O | T | L | A | K | E | 624 |
| CTT | CCG | CTG | TAC | CAC | GCA | ATG | ATG | GGT | GGC | AGT | GAG | GTG | GCC | CAG | ACC | CTC | GCC | AAG | GAG | 1872 1933 |
| T | F | A | S | T | A | S | O | L | H | S | N | V | V | N | Y | V | O | O | I | 644 |
| ACT | TTT | GCA | TCC | ACC | GCC | TCC | CAG | CTC | CAC | AGC | AAT | GTT | GTC | AAC | TAT | GTC | CAG | CAG | ATC | 1932 1993 |
| V | A | P | K | G | S | * | | | | | | | | | | | | | | 651 |
| GTG | GCA | CCC | AAG | GGC | AGT | TAG | | | | | | | | | | | | | | 1953 |

AGGCTCGTGTGATGGCCCTGCCTCTTCAGGCTCTCCAGGCTTTTCTAGATAATTGTTTGTTCCTCCAAATTCCTGTTCCC
TGATCAACTTCCTGGAGTTTATATCCCTCAGGATAATCTATTTCTCTAGCTTAGGTATCTGTGACTCTTGGGCCTCTGC
TCTGGTGGGAACCTTCTCTATAGCCCACTGAGCCCCGAGACAGAGAACCTGCCACAGCTCTCCCGCTACAGGCT
GCAGGCACTGCAGGGCAGCGGTATTCTCTCCCACTAAGTCTCTGGGAAGAAGTGAGAGGACTGATGCTCTTCTT
TTTTCTCTTCTGTCTTTTCTTGTGATTTTATGCAAGGGCTGGCATTCTGATTGTTCTTTTTCAGGTTTAAATCC
TTATTTTAATAAAGTTTCAAGCAAAAATTAAAAA

FIG. 1B.

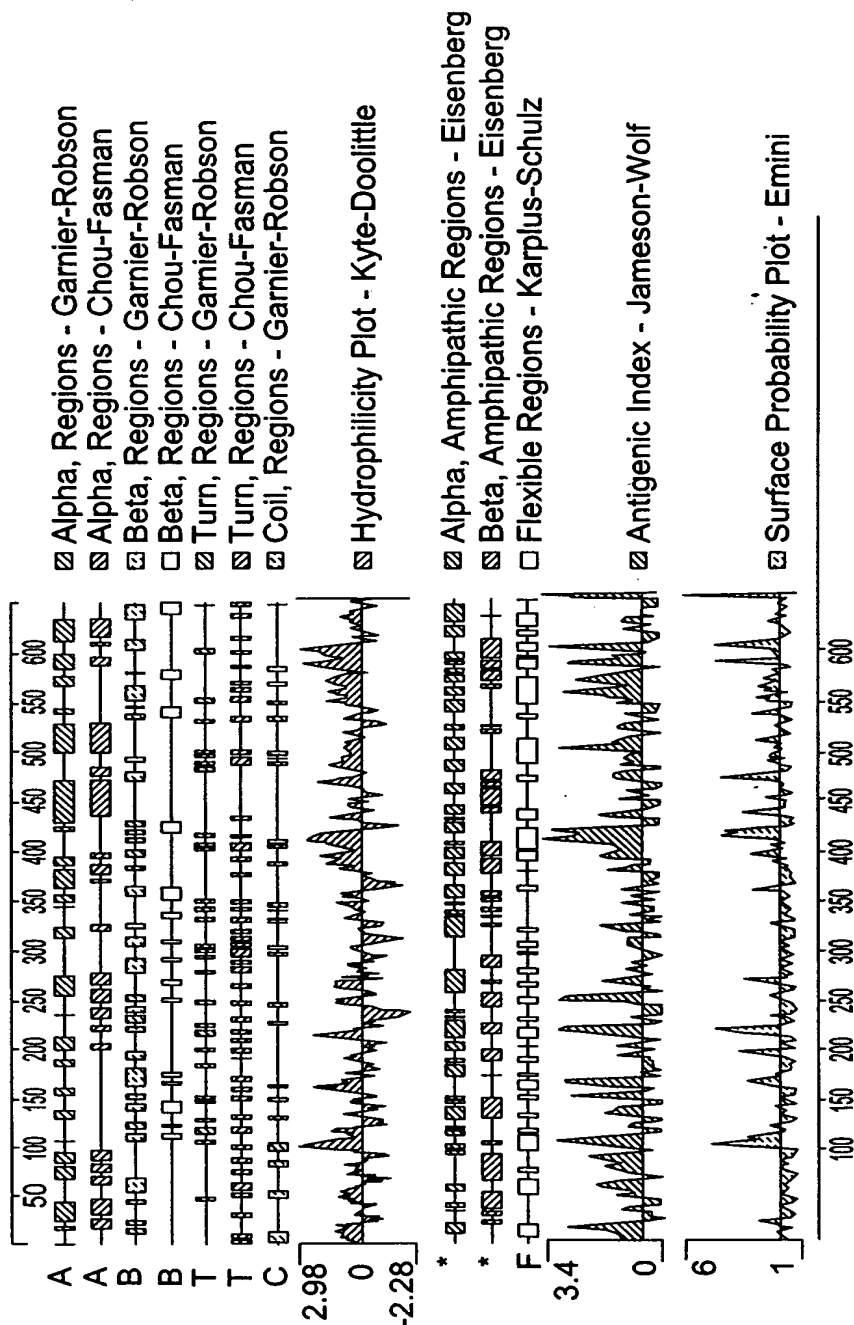


FIG. 2.

Title: 2786, A Novel Human Aminopeptidase
Inventor(s): Kapeller-Libermann et al.
Application No: Not Assigned
Atty Dkt No: 35800/242128(5800-62B)

Analysis of 2786 (650 aa)

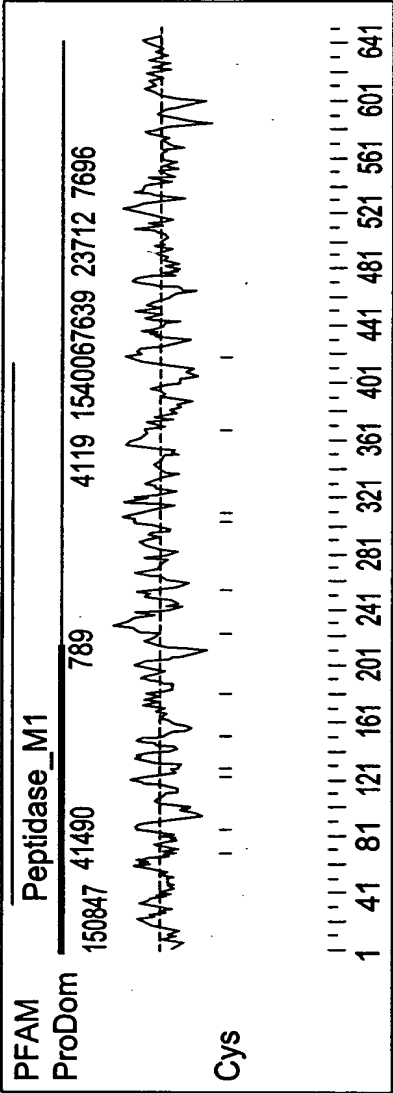


FIG. 3.

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Prosite Pattern Matches for 2786

Prosite version: Release 12.2 of February 1995

>PS00004/PDOC00004/CAMP_PHOSPHO_SITE cAMP- and cGMP-dependent protein kinase phosphorylation site.

Query: 356 RRIS 359

>PS00005/PDOC00005/PKC_PHOSPHO_SITE Protein kinase C phosphorylation site.

Query: 141 TYR 143

Query: 374 TGR 376

>PS00006/PDOC00006/CK2_PHOSPHO_SITE Casein kinase II phosphorylation site.

Query: 208 STWE 211

Analysis of 2786

Query: 318 SLAD 321

Query: 368 TCLE 371

Query: 386 TGEE 389

Query: 408 TYNE 411

Query: 412 TPYE 415

Query: 496 SPGD 499

>PS00008/PDOC00008/MYRISTYL N-myristoylation site.

Query: 9 GSGAAR 14

Query: 58 GLSGTA 63

Query: 119 GQALCV 124

Query: 333 GNLVTN 338

Query: 364 GAAYTC 369

Query: 614 GSEVAQ 619

>PS00009/PDOC00009/AMIDATION Amidation site.

Query: 159 AGKK 162

>PS00030/PDOC00030/RNP_1 Eukaryotic putative RNA-binding region RNP-1 signature.

Query: 416 KGFCFVS 423

>PS00142/PDOC00129/ZINC_PROTEASE Neutral zinc metalloproteinases, zinc-binding region signature.

Query: 322 VIIHEISHSW 331

FIG. 4.

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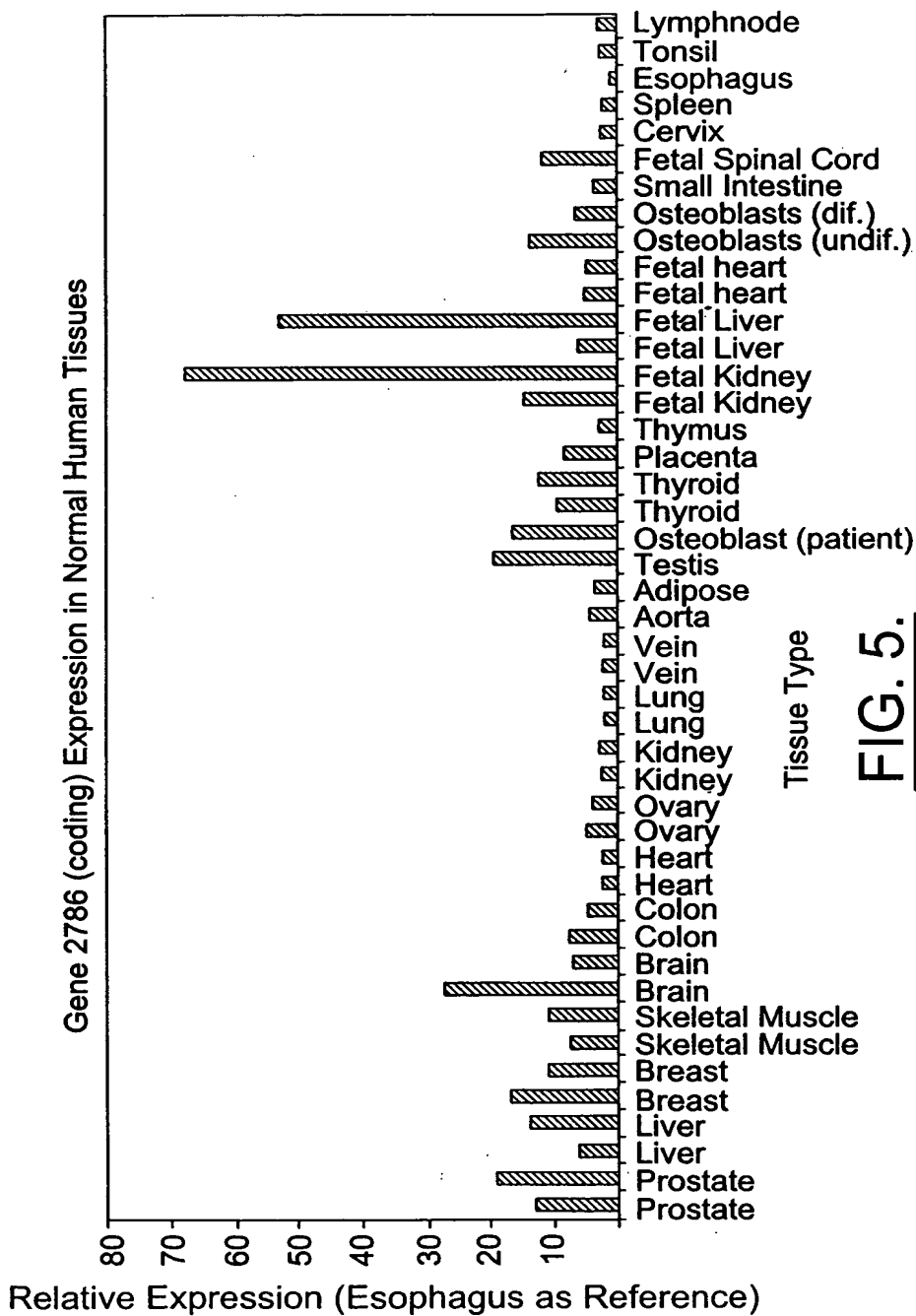


FIG. 5.

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Title: 2786, A Novel Human Aminopeptidase
 Inventor(s): Kapeller-Libermann et al.
 Application No: Not Assigned
 Atty Dkt No: 35800/242128(5800-62B)

2786 Taqman Oncology Panel

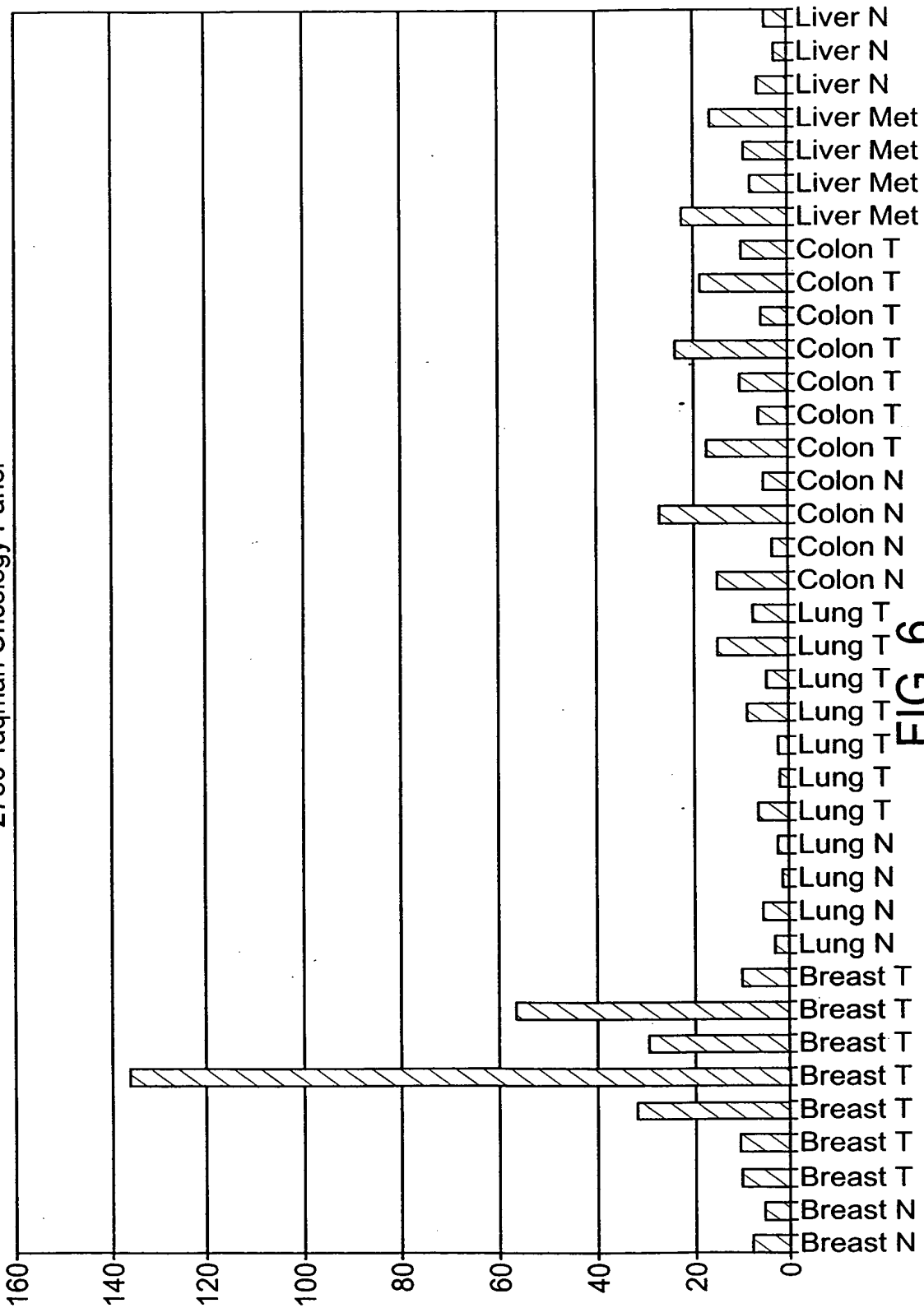


FIG. 6.

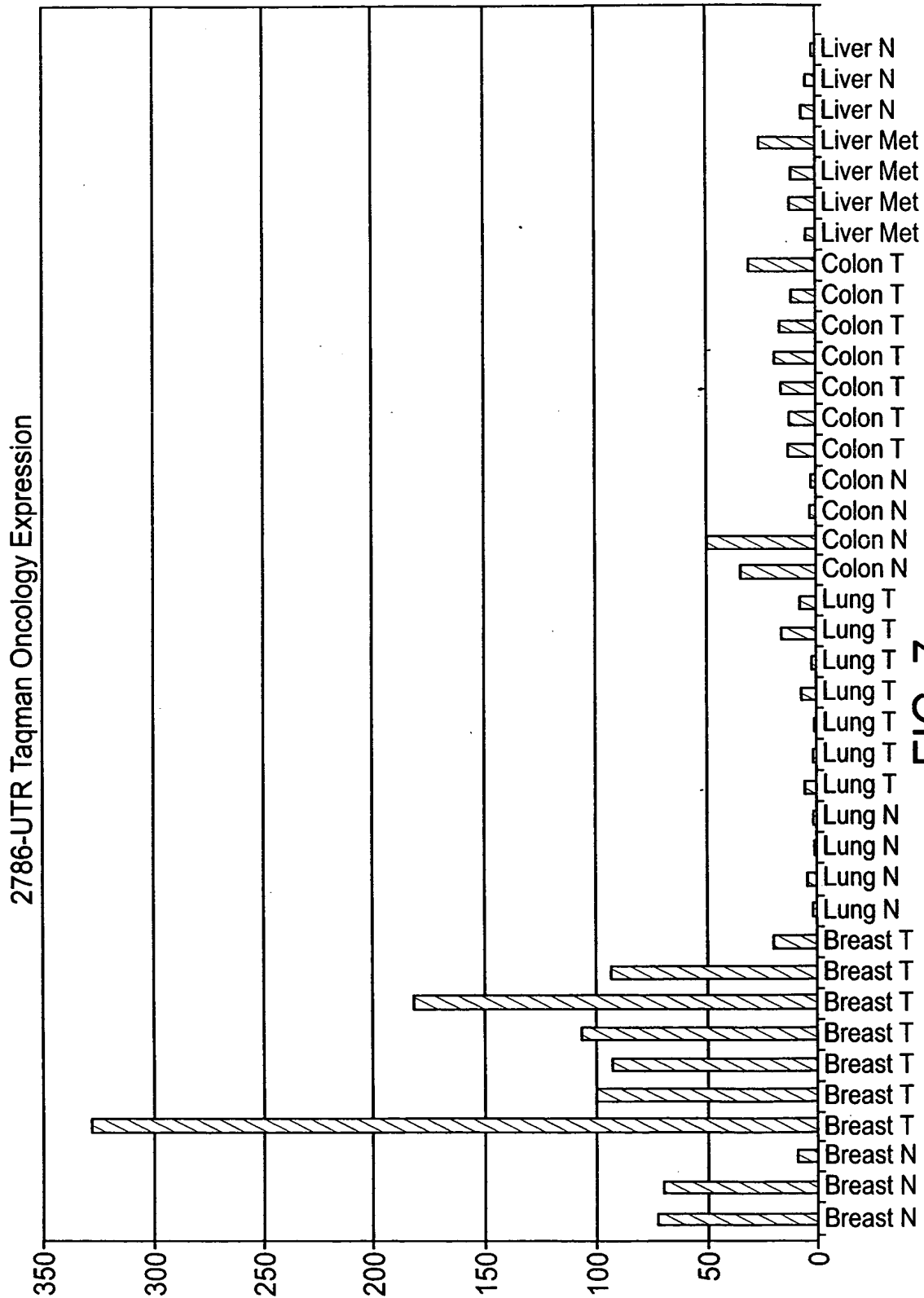


FIG. 7.

Title: 2786, A Novel Human Aminopeptidase
Inventor(s): Kapeller-Libermann et al.
Application No: Not Assigned
Atty Dkt No: 35800/242128(5800-62B)

2786 Expression in Normal Human Tissue

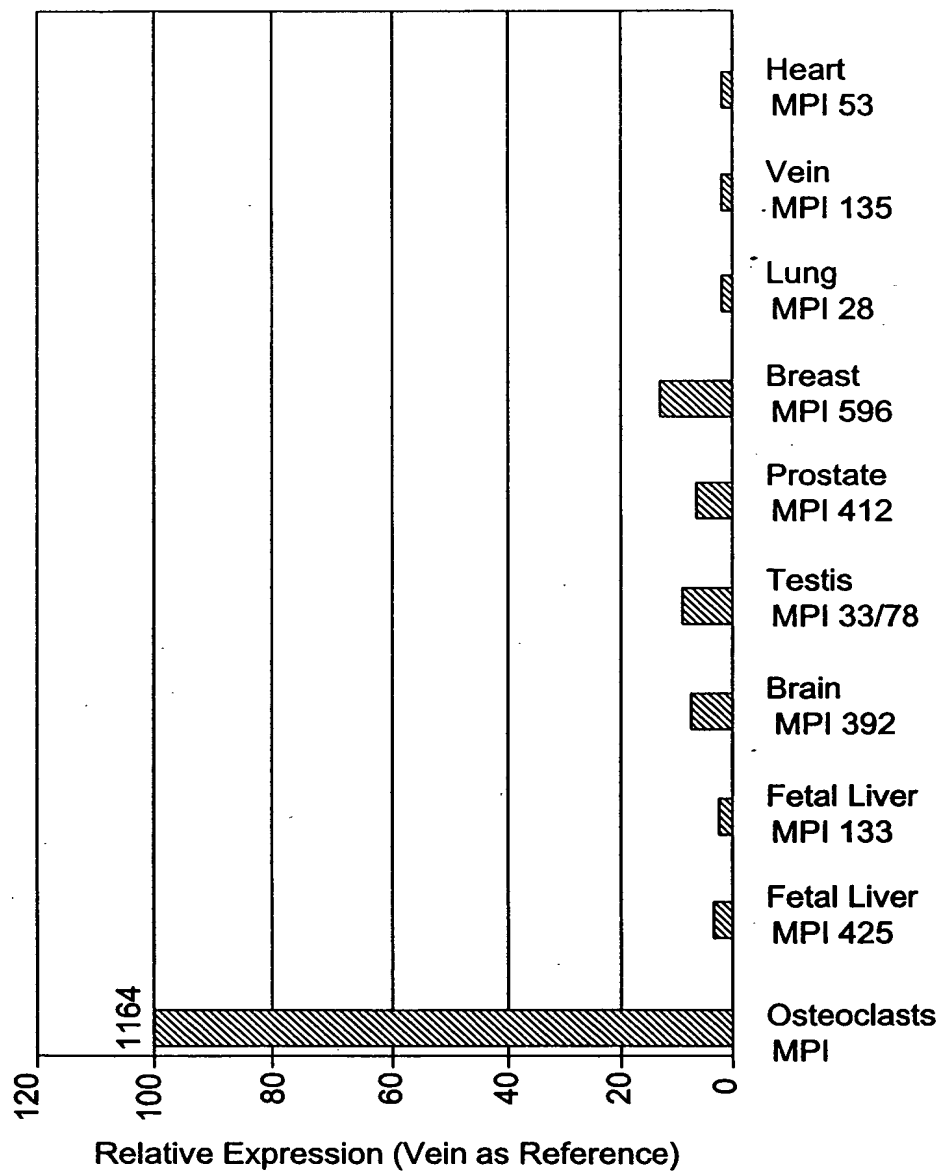


FIG. 8.